

```

1  TCCGCCCCCG GCCCAGGGTG CGAATCCGGT GCCGGCAAGC GGCTGGCGAT
51  GCTGGAGGTT CGCTAGCCGA AGCGGCTGCA TCTGGCGCCG CGTCTGCCCC
101 GCGTGCTCGG AGCGGATTCT GCCCGCCGTC CCCGGAGCCC TCGGCGCCCC
151 GCTGAGCCCG CGATCACTTC CTCCTGTGA CCAACCGGCG CTGCAGGTTA
201 GAGCCTGGCA ATGCCGTTTG GGTGTGTGAC TCTGGGCGAC AAGAAGAACT
251 ATAACCAGCC ATCGGAGGTG ACTGACAGAT ATGATTTGGG ACAGGTCATC
301 AAGACTGAGG AGTTTTGTGA AATCTTCCGG GCCAAGGACA AGACGACAGG
351 CAAGCTGCAC ACCTGCAAGA AGTTCCAGAA GCGGGACGGC CGCAAGGTGC
401 GGAAAGCTGC CAAGAACGAG ATAGGCATCC TCAAGATGGT GAAGCATCCC
451 AACATCCTAC AGCTGGTGGG TGTGTTTGTG ACCCGCAAGG AGTACTTTAT
501 CTTCTGGAG CTGGCCACGG GGAGGGAGGT GTTTGACTGG ATCCTGGACC
551 AGGGCTACTA CTCGGAGCGA GACACAAGCA ACGTGGTACG GCAAGTCCTG
601 GAGGCCGTGG CCTATTTGCA CTCACTCAAG ATCGTGCACA GGAATCTCAA
651 GCTGGAGAAC CTGGTTTACT ACAACCGGCT GAAGAACTCG AAGATTGTCA
701 TCAGTGAFTT CCATCTGGCT AAGCTAGAAA ATGGCTCAT CAAGGAGCCC
751 TGTGGGACCC CCGAGTATCT GGCCCCAGAG GTGGTAGGCC GGCAGCGGTA
801 TGGACGCCCT GTGGACTGCT GGGCCATTGG AGTCATCATG TACATCCTGC
851 TTTCAAGCAA TCCACCTTTC TATGAGGAGG TGGAAGAAGA TGATTATGAG
901 AACCATGATA AGAATCTCTT CCGCAAGATC CTGGCTGGTG ACTATGAGTT
951 TGAFTCTCCA TATTGGGATG ATATTTGCA GGCAGCCAAA GACCTGGTCA
1001 CAAGGCTGAT GGAGGTGGAG CAAGACCAGC GGATCACTGC AGAAGAGGCC
1051 ATCTCCCATG AGTGGATTTC TGGCAATGCT GCTTCTGATA AGAACATCAA
1101 GGATGGTGTG TGTGCCCAGA TTGAAAAGAA CTTTGCCAGG GCCAAGTGGA
1151 AGAAGGCTGT CCGAGTGACC ACCCTCATGA AACGGCTCCG GGCACCAGAG
1201 CAGTCCAGCA CGGCTGCAGC CCAGTCGGCC TCAGCCACAG ACACTGCCAC
1251 CCCCAGGGCT GCAGGTGGGG CCACAGCTGC AGCTGCGAGT GGAGCTACCT
1301 CAGCCCCTGA GGGTGATGCT GCTCGTGCTG CAAAGAGTGA TAATGTGGCC
1351 CCCGCAGACC GTAGTGCCAC CCCAGCCACA GATGGAAGTG CCACCCCAGC
1401 CACTGATGGC AGTGTACCCC CAGCCACCGA TGGAAGCATC ACTCCAGCCA
1451 CTGATGGGAG TGTACCCCCA GTCAGTGACA GGAGCGCTAC TCCAGCCACT
1501 GATGGGAGAG CACACCAGC CACAGAAGAG AGCACTGTGC CCACCACCCA
1551 AAGCAGTGCC ATGCTGGCCA CCAAGGCAGC TGCCACCCCT GAGCCGGCTA
1601 TGGCCCAGCC GGACAGCACA GCCCCAGAGG GCGCCACAGG CCAGGCTCCA
1651 CCCTCTAGTA AAGGGGAAGA GGCTGCTGGT TATGCCCAGG AGTCTCAAAG
1701 GGAGGAGGCC AGCTGAGTAG GCAGCTGGT GAGGGGGGGC AGGGGATGGG
1751 CAGGAGGGTG GGAGAGTGGA TGAGGGGCTT CTCAGTGTAC ATAGAGTCAC
1801 TGGCATGATG CCTCGCTCC CCCATGCCCC CACATCCCAG TGGGGCATAA
1851 CTAGGGGTCA CGGGAGAGCA GTCTCGTCTC CTGTGTGTAT GTGTGTGAGT
1901 GGTGGGCAGG CCAGTGGCAG GGCCGGCCCC AGCCCCTGCA TGGATTCTT
1951 GTGGCTTTTC TGTCTTTTGC TAGCTTCACC AGTTTCTGTT CCTTGTGGGA
2001 TGCTGCTCTA GGGATACTCA GGGGGCTCCT GCTCTCCTT CCCTTCCCTT
2051 CTTGCCCTAC CATTCCCCTA GGCAGGCCCT GCAGGTCCA CACTCTCCCA
2101 TGCCCTAAAC TTGGGCGGCC TTGCCCTGAG AGCTGGTCTT CCAGCGAGGC
2151 CCTGTCAGCG GTCTTAGGCT CCTGCACATG AAGGTGTGTG CCTGTGGTGT
2201 GTGGGCTGCT CTAGGAGCAG ATACAGGCTG GTATAGAGGA TGCAGAAAGG
2251 TAGGGCAGTA TGTTTAAGTC CAGACTTGGC ACATGGCTAG GGATACTGCT
2301 CACTAGCTGT GGAGGTCTTC AGGAGTGGAG AGAATGAGTA GGAGGGCAGA
2351 AGCTTCCATT TTTGTCCTTC CTAAGACCCT GTTATTTGTG TTATTTCTTG
2401 CCTTTCCGAG TCCTGCAGTG GGCTGCCCTG TACCCTGAAC CTCATGAGCC
2451 TCTAAGGGAA AGGAGGAACA ATTAGGACGT GGCAATGAGA CCTGGCAGGG
2501 CAGAGTACAA GCCCAGCACC CAGTGTCCCA GCCTTACTGG GTCCTTACCC
2551 TGGGCCAAAC AGGGAGGGCT GATACCTCCT TGCTCTTCT AGATGCCAC
2601 CTCCTACAAT CTCAGCCCAC AAGTCCTCTC CACCCTAGGG GGCTTGCTGC
2651 ATGGCAATAA CTCATAATCT GATTGGAGG TTTGCCCTT ACAGGGGCAG
2701 ATTTTCTGCT CAGTTCAACA ATGAAATGAA GAGGAAGTCC CTCTTTCTAC
2751 AGCTCACTTC TATCAGAGGC CCAGGTGCCT CAGAGCCACA TTGAGTTGCT
2801 TTTTCTGGGA TGAGGAAGTA GGGTTAACT CCCAGTTTC CTGAGGGAGG
2851 CTCCTGACAG GTGCCCTTTG TCAGACCCTA CCACAGCCTG GATAGGCAGC
2901 CACATTGGTC CTCGCCCTTG CTCGGCACTC CGTGGTGGTC CTGCCCTTCT

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FIGURE 1A

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2951 CCCTGCATGC CTGTGGGTCT GCTCTGGTGT GTGAAGGTCG GTGGGTTAAC
3001 TGTGTGCCTA CTGAACCTGG CAAATAAACA TCACCCTGCA AAGCCAAAAA
3051 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3101 AAAAAAAAAA AAAAAAAAAA AAAA

```

FEATURES:

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5'UTR:      1 - 210
Start Codon: 211
Stop Codon:  1714
3'UTR:      1717

```

Homologous proteins:

Top 10 BLAST Hits

	Score	E
gi 2143639 pir I56542 calmodulin-binding protein - rat >gi 349...	929	0.0
gi 7521914 pir T30814 calmodulin-binding protein kinase - Fugu...	598	e-170
gi 3122310 sp Q63450 KCCL_RAT CALCIUM/CALMODULIN-DEPENDENT PROT...	310	4e-83
gi 4502553 ref NP_003647.1 calcium/calmodulin-dependent protei...	309	9e-83
gi 3114436 pdb 1A06 Calmodulin-Dependent Protein Kinase Fro...	303	7e-81
gi 406113 gb AAA19670.1 (L24907) protein kinase I [Rattus norv...	299	1e-79
gi 9966875 ref NP_065130.1 CamKI-like protein kinase [Homo sap...	299	1e-79
gi 3893099 emb CAA76937.1 (Y17917) calcium/calmodulin dependen...	288	3e-76
gi 4007153 emb CAA19296.1 (AL023754) dJ272L16.1 (Rat Ca2+/Calmodu...	286	1e-75
gi 4678722 emb CAB41259.1 (AL049688) hypothetical protein [Hom...	286	1e-75

BLAST to dbEST:

	Score	E
gi 11264319 /dataset=dbest /taxon=96...	1057	0.0
gi 11126214 /dataset=dbest /taxon=96...	989	0.0
gi 11259094 /dataset=dbest /taxon=96...	963	0.0
gi 11260705 /dataset=dbest /taxon=96...	896	0.0
gi 708663 /dataset=dbest /taxon=9606 /...	611	e-172
gi 10215012 /dataset=dbest /taxon=96...	601	e-169
gi 11099650 /dataset=dbest /taxon=960...	577	e-162
gi 831534 /dataset=dbest /taxon=9606 /...	535	e-150
gi 9136656 /dataset=dbest /taxon=9606...	529	e-148
gi 2001736 /dataset=dbest /taxon=9606 ...	509	e-142

EXPRESSION INFORMATION FOR MODULATORY USE:

Library source:

Expression information from BLAST dbEST hits:

```

gi|11264319 Brain
gi|11126214 Lung
gi|11259094 Brain
gi|11260705 Brain
gi|708663 Infant brain
gi|10215012 Lung
gi|11099650 Brain
gi|831534 Infant brain
gi|9136656 Brain
gi|2001736 Infant brain

```

Expression information from PCR-based tissue screening panels:

Infant brain, hippocampus

FIGURE 1B

```

1 MPFGCVTLGD KKNYNQPSEV TDRYDLGQVI KTEEFCEIFR AKDKTTGKLH
51 TCKKFQKRDG RKVRKAAKNE IGILKMKHP NILQLVDVFN TRKEYFIFLE
101 LATGREVFDW ILDQGYYSER DTSNVVRQVL EAVAYLHSLK IVHRNLKLEN
151 LVYYNRLKNS KIVISDFHLA KLENGLIKEP CGTPEYLAPE VVGRQRYGRP
201 VDCWAIGVIM YILLSGNPPF YEEVEEDDYE NHDKNLFRKI LAGDYEFDSP
251 YWDDISQAAK DLVTRLMEVE QDQRITAEAA ISHEWISGNA ASDKNIKDGV
301 CAQIEKNFAR AKWKKAVRVT TLMKRLRAPE QSSTAAQAQA SATDTATPGA
351 AGGATAAAAS GATSAPEGDA ARAAKSDNVA PADRSATPAT DGSATPATDG
401 SVTPATDGTI TPATDGSVTP VTDRSATPAT DGRATPATTEE STVPTTQSSA
451 MLATKAAATP EPAMAQPDST APEGATGQAP PSSKGEEAAG YAQESQREEA
501 S

```

FEATURES:

Functional domains and key regions:

[1] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 11

```

1      21-23 TDR
2      422-424 TDR
3      46-48 TGK
4      51-53 TCK
5      91-93 TRK
6      103-105 TGR
7      118-120 SER
8      138-140 SLK
9      292-294 SDK
10     21-23 TDR
11     422-424 TDR

```

[2] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 10

```

1      7-10 TLGD
2      91-94 TRKE
3      103-106 TGRE
4      118-121 SERD
5      276-279 TAEE
6      341-344 SATD
7      364-367 SAPE
8      470-473 TAPE
9      483-486 SKGE
10     495-498 SQRE

```

[3] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

Number of matches: 2

```

1      127-135 RQVLEAVAY
2      484-491 KGEEAAGY

```

FIGURE 2A

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 4

1	288-293	GNAASD
2	349-354	GAAGGA
3	352-357	GGATAA
4	353-358	GATAAA

[5] PDOC00009 PS00009 AMIDATION
Amidation site

59-62 DGRK

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	207	227	1.342	Certain
2	351	371	1.250	Certain

BLAST Alignment to Top Hit:

>gi|2143639|pir||I56542 calmodulin-binding protein - rat
gb|AAA16633.1| (L22557) calmodulin-binding protein [Rattus norvegicus]
Length = 504

Score = 929 bits (2375), Expect = 0.0
Identities = 468/509 (91%), Positives = 473/509 (91%), Gaps = 8/509 (1%)
Frame = +1

Query: 211 MPFGCVTLGDKKNYNQPSVETDRYDLGQVIKTEEFCEIFRAKDKTGKLTCKKFQKRDG 390
MPFGCVTLGDKKNYNQPSVETDRYDLGQV+KTEEFCEIFRAKDKTGKLTCKKFQKRDG
Sbjct: 1 MPFGCVTLGDKKNYNQPSVETDRYDLGQWKTEEFCEIFRAKDKTGKLTCKKFQKRDG 60

Query: 391 RKVRKAAKNEIGILKMVKHPNQLVDFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
RKVRKAAKNEIGILKMVKHPNQLVDFVTRKEYFIFLELATGREVFDWILDQGYYSER
Sbjct: 61 RKVRKAAKNEIGILKMVKHPNQLVDFVTRKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571 DTSNVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 750
DTSNVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP
Sbjct: 121 DTSNVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 180

Query: 751 CGTPEYLAPEVWGRQRYGRPVDQWAIQVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
CGTPEYLAPEVWGRQRYGRPVDQWAIQVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI
Sbjct: 181 CGTPEYLAPEVWGRQRYGRPVDQWAIQVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 240

Query: 931 LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDG 1110
LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDG
Sbjct: 241 LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDG 300

Query: 1111 CAQIEKNFARAKWKAVRVTTLMKRLRAPEQSSTAAASASATDTATPGAAGGATAAAAS 1290
CAQIEKNFARAKWKAVRVTTLMKRLRAPEQS TAA +D ATPGAAGGA AAAA
Sbjct: 301 CAQIEKNFARAKWKAVRVTTLMKRLRAPEQSGTAA-----TSDAATPGAAGGAVAAAAG 355

Query: 1291 G-----ATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSITP 1446
G AT GDA AAKSD++A ADRSATPATDGSATPATDGSVTPATDGSITP
Sbjct: 356 GAAPASGASATVGTGGDAGCAAKSDDMASADRSATPATDGSATPATDGSVTPATDGSITP 415

FIGURE 2B

Query: 1447 ATDGSVTPVTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAP 1626
 ATDGSVTP TDRSATPATDGRATPATEESTVP QSSA A KAAATPEPA+AQPDSTA
 Sbjct: 416 ATDGSVTPATDRSATPATDGRATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTAL 475

Query: 1627 EGATGQAPPSSKGEEAAGYAQESQREEAS 1713
 EGATGQAPPSSKGEEA G AQESQR E S
 Sbjct: 476 EGATGQAPPSSKGEEATGCAQESQRVETS 504

Score = 34.4 bits (77), Expect = 7.1
 Identities = 42/158 (26%), Positives = 60/158 (37%), Gaps = 5/158 (3%)
 Frame = -3

Query: 1673 ASSPLLEGGAWPVAPSGAVLSGWAIA--GSGVAAALVASMALLWVGTVLSSVAGVALPS 1500
 A++P GGA A GA + A A G+G A A ++S A P+
 Sbjct: 340 AATPGAAGGAVAAAAGGAAPASGASATVGTGGDAGCAAK-----SDDMASADRSATPA 392

Query: 1499 VAGVALLSVTGVTLPSVAGVMLPSVAGVTLPSVAGVALPSVAGVALRSAGATLSLFAARA 1320
 G A + G P+ G + P+ G P+ A P+ G
 Sbjct: 393 TDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDG-----R 436

Query: 1319 ASPSGAEVAPLAAAAVAPPAAPGVAV---SVAEADWAA 1215
 A+P+ E AA + A PAA A +VA+ D A
 Sbjct: 437 ATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTA 474

>gi|7521914|pir||T30814 calmodulin-binding protein kinase - Fugu
 rubripes
 emb|CAA09101.1| (AJ010348) calmodulin binding protein kinase [Fugu rubripes]
 Length = 421

Score = 598 bits (1526), Expect = e-170
 Identities = 296/391 (75%), Positives = 332/391 (84%), Gaps = 2/391 (0%)
 Frame = +1

Query: 211 MPFGCVTLGDKKNYNQPSSEVTDTRYDLGQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDG 390
 MPFGC+TLG+KK+YN PSEVTD+YDLGQV+K+EEFCEIFRAKD+ T K++TCKKF K+DG
 Sbjct: 1 MPFGCLTLGEKKDYNPSEVTDKYDLGQVWKSEEFCEIFRAKDRNTLKMYTCKKFNKKDG 60

Query: 391 RKVRKAAKNEIGILKMVKHPNQLVDFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
 RKVRKAAKNEI ILKMVKH NILQLVD F T+KEYFIFLELATGREVFDWILDQGYYSER
 Sbjct: 61 RKVRKAAKNEIMILKMVKHHNILQLVDAFETKKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571 DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP 750
 DTSNV+RQVLEAVAYLHSLKIVHRNLK NLVY+NRLLK+SKIVISDF LAKLENGLIK+P
 Sbjct: 121 DTSNMRQVLEAVAYLHSLKIVHRNLK--NLVYFNRLKHKIVISDFQLAKLENGLIKDP 178

Query: 751 CGTPEYLAPEVWGRQRYGRPVDQWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
 CGTPEYLAPEV+GRQRYGRPVDQWAIGVIMYILLSGNPPFY++ +E+D ++ DKNLF KI
 Sbjct: 179 CGTPEYLAPEVIGRQRYGRPVDQWAIGVIMYILLSGNPPFYDDGDEEDSDSRDKNLFLKI 238

Query: 931 LAGDYEFDSPYWDDISQAADLVTRLMEVEQDQRITAEAEISHWISGNAASDKNIKDGV 1110
 L+GDYEFDSPYWDDIS +AK LV LMEV+QDQR+TA+EAI+HEWISGNAASDKNIKDGV
 Sbjct: 239 LSGDYEFDSPYWDDISDSAKTLVASLMEVDQDQRLTAQEATAHEWISGNAASDKNIKDGV 298

FIGURE 2C

Query: 1111 CAQIEKNFARAKWKAVRVTTLMKRLRAPEQSSTAAQASAT--DTATPGAAGGATAAA 1284
 CAQIEKNFA+AKWKAVRVTTLMKRLRA EQ T A+ A+ P GG+ AA
 Sbjct: 299 CAQIEKNFAKAKWKAVRVTTLMKRLRASEQGDGTGASGLAAGATGGPPDPNMPGGSLLAA 358

Query: 1285 ASGATSAPEGDAARAASDNVAPADRSATPA 1377
 + + A S+ A A S P+
 Sbjct: 359 -----SIKTALSEKAADAQTSTIPS 378

>gi|3122310|sp|Q63450|KCC1_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN
 KINASE TYPE I (CAM KINASE I)
 pir||S50193 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
 gb|AAA66944.1| (L26288) Cam-like protein kinase [Rattus norvegicus]
 prf||2024225A Ca/calmodulin protein kinase I [Rattus norvegicus]
 Length = 374

Score = 310 bits (787), Expect = 4e-83
 Identities = 156/357 (43%), Positives = 226/357 (62%), Gaps = 4/357 (1%)
 Frame = +1

Query: 250 YNQPSEVTDRLQGVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
 + Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
 Sbjct: 10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIIV 69

Query: 430 LKMKHPNIIQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
 L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
 Sbjct: 70 LHKIKHPNIIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610 AYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAP 783
 YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
 Sbjct: 130 KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPY 963
 + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPY
 Sbjct: 190 LAQKPYSKAVDCWSIGVIAIYILLCGYPPFYDE-----NDAKLFEQILKAIEYEFDSPY 241

Query: 964 WDDISQAAKDLVTRLMEVEQDQRITAEAEISHEWISGNAASDKNIKDGVCQIEKNFARA 1143
 WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
 Sbjct: 242 WDDISDSAKDFIRHLMKDPKRFTEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKAVRVTTLMKRLRAPE--QSSTAAQASATDTATPGAAGGATAAAASGATSAP 1308
 KWK+A T +++ +R + S Q+AS + TP A G A P
 Sbjct: 302 KWKQAFNATAVVRHMRKLQLGTSQEQGQTASHGELLTPTAGGPAAGCCCRDCCVEP 358

>gi|4502553|ref|NP_003647.1| calcium/calmodulin-dependent protein
 kinase I [Homo sapiens]
 sp|Q14012|KCC1_HUMAN CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (CAM KINASE I)
 pir||S57347 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
 gb|AAA99458.1| (L41816) cam kinase I [Homo sapiens]
 Length = 370

Score = 309 bits (784), Expect = 9e-83
 Identities = 156/357 (43%), Positives = 225/357 (62%), Gaps = 4/357 (1%)
 Frame = +1

FIGURE 2D

```

Query: 250 YNQPSVTDRLDGLGVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
          + Q ++ D YD V+ T F E+ A+DK T KL K K + +NEI +
Sbjct: 10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEGSMENEIAY 69

Query: 430 LKMMKHPNIIQLVDVFTVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
          L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610 AYLSLKIIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
          YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
Sbjct: 130 KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPY 963
          + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPY
Sbjct: 190 LAQKPYSKAVDQWSIGVIAYILLCGYPPFYDE-----NDAKLFEQILKAIEYEFDSPY 241

Query: 964 WDDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQIEKNFARA 1143
          WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
Sbjct: 242 WDDISDSAKDFIRHLMKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKA VRVTTLMKRLRAPE--QSSTAAAQSASATDTATPGAAGGATAAAAASGATSAP 1308
          KWK+A T +++ +R + S Q+AS + TP A G A P
Sbjct: 302 KWKQAFNATAWRHMRKLQLGTSQEGQGQTASHGELLTPVAGGPAAGCCCRDCCVEP 358

```

>gi|3114436|pdb|1A06| Calmodulin-Dependent Protein Kinase From Rat
Length = 332

Score = 303 bits (768), Expect = 7e-81
Identities = 146/316 (46%), Positives = 213/316 (67%), Gaps = 2/316 (0%)
Frame = +1

```

Query: 250 YNQPSVTDRLDGLGVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
          + Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
Sbjct: 10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAY 69

Query: 430 LKMMKHPNIIQLVDVFTVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
          L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610 AYLSLKIIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
          YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
Sbjct: 130 KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPY 963
          + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPY
Sbjct: 190 LAQKPYSKAVDQWSIGVIAYILLCGYPPFYDE-----NDAKLFEQILKAIEYEFDSPY 241

Query: 964 WDDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQIEKNFARA 1143
          WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
Sbjct: 242 WDDISDSAKDFIRHLMKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKA VRVTTLMKRLR 1191
          KWK+A T +++ +R
Sbjct: 302 KWKQAFNATAWRHMR 317

```

FIGURE 2E

>gi|406113|gb|AAA19670.1| (L24907) protein kinase I [Rattus
norvegicus]
Length = 332

Score = 299 bits (758), Expect = 1e-79
Identities = 146/316 (46%), Positives = 212/316 (66%), Gaps = 2/316 (0%)
Frame = +1

Query: 250 YNQPSEVTDRLGQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
+ Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
Sbjct: 10 WKQAEIDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEI 69

Query: 430 LKMVKHPNIIQLVDVFTTRKEYFIFLELATGREVFDWILDQGYSERDTSNVRQVLEAV 609
L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G Y+ERD S ++ QVL+AV
Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGGYTERDRSRLIFQVLDAV 129

Query: 610 AYLSLKIIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
Sbjct: 130 KYLHDLGIVHRDLKPENLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPI 963
+ ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPI
Sbjct: 190 LAQKPYSKAVDCWSIGVIAIYILLCGYPPFYDE-----NDAKLFEQILKAEYEFDSPI 241

Query: 964 WDDISQAAKDLVTRLMEVEQDQRITAEAEISHEWISGNAASDKNIKDGVCQIEKNFARA 1143
WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
Sbjct: 242 WDDISDSAKDFIRHLMKDPKRFRTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKAVRVTTLMKRLR 1191
KWK+A T +++ +R
Sbjct: 302 KWKQAFNRTAVVRHMR 317

>gi|9966875|ref|NP_065130.1| CamKI-like protein kinase [Homo sapiens]
gb|AAG00534.1|AF286366_1 (AF286366) CamKI-like protein kinase [Homo sapiens]
Length = 357

Score = 299 bits (757), Expect = 1e-79
Identities = 142/332 (42%), Positives = 221/332 (65%), Gaps = 2/332 (0%)
Frame = +1

Query: 256 QPSEVTDRLGQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
Q ++ ++ + + T F E+ A++K TGKL K K+ + + +NEI +L+
Sbjct: 15 QAEDIKKIIFFKETLGTGAFSEVLAEEKATGKLFAVKCIPKKALKGKESSIENEI 74

Query: 436 MVKHPNIIQLVDVFTTRKEYFIFLELATGREVFDWILDQGYSERDTSNVRQVLEAVAY 615
+KH NI+ L D++ + ++ ++L +G E+FD I+++G+Y+E+D S ++RQVL+AV Y
Sbjct: 75 KIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAVY 134

Query: 616 LHSLKIIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLE--NGLIKEPCGTPEYLAPEVWG 789
LH + IVHR+LK ENL+YY++ + SKI+ISDF L+K+E ++ CGTP Y+APEV+
Sbjct: 135 LHRMGIVHRDLKPENLLYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVLA 194

Query: 790 RQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPIWD 969
++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPIWD
Sbjct: 195 QKPYSKAVDCWSIGVIAIYILLCGYPPFYDE-----NDSKLFEQILKAEYEFDSPIWD 246

FIGURE 2F

Query: 970 DISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCAQIEKNFARAKW 1149
 DIS +AKD + LME + ++R T E+A H WI+G+ A +KNI + V AQI KNFA++KW
 Sbjct: 247 DISDSAKDFIRNLMEKDPNKRYTCEQAARHPWJAGDTALNKNIHESVSAQIRKNFAKSKW 306

Query: 1150 KKAVRVTTLMKRLRAPEQSSTAAASASATDT 1245
 ++A T +++ +R S+ + +AS + +
 Sbjct: 307 RQAFNATAVVRHMRKLHLGSSLDSSNASVSSS 338

>gi|3893099|emb|CAA76937.1| (Y17917) calcium/calmodulin dependent
 protein kinase I [Drosophila melanogaster]
 gb|AAF59343.1| (AE003844) CaMKI gene product [alt 2] [Drosophila melanogaster]
 Length = 405

Score = 288 bits (729), Expect = 3e-76
 Identities = 152/388 (39%), Positives = 243/388 (62%), Gaps = 21/388 (5%)
 Frame = +1

Query: 238 DKKNYNQPSVETDRYDLGQVIKTEEFCEIFRAKDKTT-GKLHTCKKFQKRDGRKVRKAAK 414
 D K N+ + ++Y+L ++ T F E+ A+ K + G+ K K+ + ++ +
 Sbjct: 17 DLKELNKQVSIEEKYNLHGLLGTGAFSEVRLAESKDSPEHFVAVKIIDKKALKGKEESLE 76

Query: 415 NEIGILKM-----VKHPNIIQLVDVFTVTRKEYFIFLELATGREVDFWILD 549
 NEI +L+ + HPNI+QL++ + + + ++ +EL TG E+FD I++
 Sbjct: 77 NEIRVLRFRFSANHFDDGKCLNGTRLTHPNIVQLLETIEDKSKVYLMELVTGGELFDRIVE 136

Query: 550 QGYYSERDTSNVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLE 729
 +G Y+E+D S+++RQ+LEAV Y+H +VHR+LK ENL+YY+ +SKI+ISDF L+K+E
 Sbjct: 137 KGSYTEKDASHLIRQILEAVDYMHEQGVVHRDLKPENLLYSPDDDSKIMISDFGLSKME 196

Query: 730 N-GLIKEPCGTPEYLAPEVWGRQRYGRPVDQWAGVIMYILLSGNPPFYEEVEEDDYENH 906
 + G++ CGTP Y+APEV+ ++ YG+ VD W+IGVI YILL G PPFY+E +
 Sbjct: 197 DSGIMATACGTPGYVAPEVLAQKPYGKAVDWSIGVISYILLCGYPPFYDE-----N 248

Query: 907 DKNLFRKILAGDYEFDSPYWDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAAS 1086
 D NLF +IL GD+EFDSPYWD+IS++AK + LM V ++R T ++A+ H WISGN AS
 Sbjct: 249 DANLFAQILKGFEDDSPYWDEISESAKHFIKNLMCVTEKRYTCKQALGHAWISGNEAS 308

Query: 1087 DKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAA-----QSASATDTATP 1254
 +NI V Q++KNFA+++WK+A T+++++ +S + A ++S D+ TP
 Sbjct: 309 SRNIHGTVSEQLKKNFAKSRWKQAYYAATVIRQMQRMALNSNSNANFDSSNSSNQDSTTP 368

Query: 1255 GAAGGATAAAASGATSAPEGDAARAAS 1338
 AA GA + + + + A KS
 Sbjct: 369 TAATGAWTSNVLSSQQSVQSHAQEMNKS 396

>gi|4007153|emb|CAA19296.1| (AL023754) dJ272L16.1 (Rat Ca²⁺/Calmodulin
 dependent Protein Kinase LIKE protein) [Homo sapiens]
 Length = 460

Score = 286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256 QPSEVTDYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
 Q + + + +V+ + F E+F K + TGKL K +K + + +NEI +LK
 Sbjct: 15 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLK 73

FIGURE 2G

Query: 436 MVKHPNIIQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAVAY 615
 +KH NI+ L D++ + Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
 Sbjct: 74 KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILRGVYTEKDASLVIQQVLSAVKY 133

Query: 616 LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVWGR 792
 LH IVHR+LK ENL+Y +NSKI+I+DF L+K+E NG++ CGTP Y+APEV+ +
 Sbjct: 134 LHENGIVHRDLKPENLLYLTPPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 193

Query: 793 QRYGRPVDQWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPYWDD 972
 + Y + VDW+IGVI YILL G PPFYEE E LF KI G YEF+SP+WDD
 Sbjct: 194 KPYSKAVDQWSIGVITYILLCGYPPFYETE-----SKLFEKIKEGYEFESPFWDD 245

Query: 973 ISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQIEKNFARAKWK 1152
 IS++AKD + L+E + ++R T E+A+SH WI GN A ++I V QI+KNFA++KW+
 Sbjct: 246 ISESAKDFICHILLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 305

Query: 1153 KAVRVTTLMKRLRAPEQS--STAAAQSASATDTATPGAAGGATAAAAASGATSAPGDAAR 1326
 +A ++ +R + S T + ++ T AP D +
 Sbjct: 306 QAFNAAVWHMRKLHMLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 365

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
 A + P P G S +GS+ S+ P GS+
 Sbjct: 366 ALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 411

>gi|4678722|emb|CAB41259.1| (AL049688) hypothetical protein [Homo sapiens]
 Length = 481

Score = 286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256 QPSEVTDRLDGLQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
 Q + + + +V+ + F E+F K + TGKL K +K + + +NEI +LK
 Sbjct: 20 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKSPAFR-DSSLENETAVLK 78

Query: 436 MVKHPNIIQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAVAY 615
 +KH NI+ L D++ + Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
 Sbjct: 79 KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILRGVYTEKDASLVIQQVLSAVKY 138

Query: 616 LHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVWGR 792
 LH IVHR+LK ENL+Y +NSKI+I+DF L+K+E NG++ CGTP Y+APEV+ +
 Sbjct: 139 LHENGIVHRDLKPENLLYLTPPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 198

Query: 793 QRYGRPVDQWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPYWDD 972
 + Y + VDW+IGVI YILL G PPFYEE E LF KI G YEF+SP+WDD
 Sbjct: 199 KPYSKAVDQWSIGVITYILLCGYPPFYETE-----SKLFEKIKEGYEFESPFWDD 250

Query: 973 ISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQIEKNFARAKWK 1152
 IS++AKD + L+E + ++R T E+A+SH WI GN A ++I V QI+KNFA++KW+
 Sbjct: 251 ISESAKDFICHILLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 310

Query: 1153 KAVRVTTLMKRLRAPEQS--STAAAQSASATDTATPGAAGGATAAAAASGATSAPGDAAR 1326
 +A ++ +R + S T + ++ T AP D +
 Sbjct: 311 QAFNAAVWHMRKLHMLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 370

FIGURE 2H

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
 A + P P G S +GS+ S+ P GS+
 Sbjct: 371 ALPALTQLPCQHGRRTAPGGRSLNCLVNGSL--HISSSLVPMHQSL 416

>gi|2143639|pir||I56542 calmodulin-binding protein - rat
 gb|AAA16633.1| (L22557) calmodulin-binding protein [Rattus norvegicus]
 Length = 504

Score = 929 bits (2375), Expect = 0.0
 Identities = 468/509 (91%), Positives = 473/509 (91%), Gaps = 8/509 (1%)
 Frame = +1

Query: 211 MPFGCVTLGDKKNYNQPSVETDRYDLGQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDG 390
 MPFGCVTLGDKKNYNQPSVETDRYDLGQV+KTEEFCEIFRAKDKTGKLHTCKKFQKRDG
 Sbjct: 1 MPFGCVTLGDKKNYNQPSVETDRYDLGQVWKTEEFCEIFRAKDKTGKLHTCKKFQKRDG 60

Query: 391 RKVRKAAKNEIGILKMVKHPNIIQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
 RKVRKAAKNEIGILKMVKHPNIIQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER
 Sbjct: 61 RKVRKAAKNEIGILKMVKHPNIIQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571 DTSNVVRQMLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP 750
 DTSNVVRQMLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP
 Sbjct: 121 DTSNVVRQMLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP 180

Query: 751 CGTPEYLAPEVWGRQRYGRPVDQWAIQVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 930
 CGTPEYLAPEVWGRQRYGRPVDQWAIQVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI
 Sbjct: 181 CGTPEYLAPEVWGRQRYGRPVDQWAIQVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKI 240

Query: 931 LAGDYEFDSPYWDDISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDG 1110
 LAGDYEFDSPYWDDISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDG
 Sbjct: 241 LAGDYEFDSPYWDDISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDG 300

Query: 1111 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAQASATDTATPGAAGGATAAAAS 1290
 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQS TAA +D ATPGAAGGA AAAA
 Sbjct: 301 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSGTAA-----TSDAATPGAAGGAVAAAAG 355

Query: 1291 G-----ATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSITP 1446
 G AT GDA AAKSD+HA ADRSATPATDGSATPATDGSVTPATDGSITP
 Sbjct: 356 GAAPASGASATVGTGGDAGCAAKSDDMASADRSATPATDGSATPATDGSVTPATDGSITP 415

Query: 1447 ATDGSVTPVTD RSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAP 1626
 ATDGSVTP TDRSATPATDGRATPATEESTVP QSSA A KAAATPEPA+AQPDSTA
 Sbjct: 416 ATDGSVTPATDRSATPATDGRATPATEESTVPAAQSSAAPAKAAATPEPAVAQPDSTAL 475

Query: 1627 EGATGQAPPSSKGEEAAGYAQESQREEAS 1713
 EGATGQAPPSSKGEEA G AQESQR E S
 Sbjct: 476 EGATGQAPPSSKGEEATGCAQESQRVETS 504

Score = 34.4 bits (77), Expect = 7.1
 Identities = 42/158 (26%), Positives = 60/158 (37%), Gaps = 5/158 (3%)
 Frame = -3

Query: 1673 ASSPLLEGAWPVAPSGAVLSGWAIA--GSGVAAALVASMALLWWVGTVLSSVAGVALPS 1500
 A++P GGA A GA + A A G+G A A ++S A P+
 Sbjct: 340 AATPGAAGGAVAAAAGGAAPASGASATVGTGGDAGCAAK-----SDDMASADRSATPA 392

FIGURE 2I

Query: 1499 VAGVALLSVTGVTLPSVAGVMLPSVAGVTLPSVAGVALPSVAGVALRSAGATLSLFAARA 1320
 G A + G P+ G + P+ G P+ A P+ G
 sbjct: 393 TDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDG-----R 436

Query: 1319 ASPSGAEVAPLAAAAPPAAPGVAV---SVAEADWAA 1215
 A+P+ E AA + A PAA A +VA+ D A
 sbjct: 437 ATPATEESTVPAAQSSAAPAAKAAATPEPAVAQPDSTA 474

>gi|7521914|pir||T30814 calmodulin-binding protein kinase - Fugu
 rubripes
 emb|CAA09101.1| (AJ010348) calmodulin binding protein kinase [Fugu rubripes]
 Length = 421

Score = 598 bits (1526), Expect = e-170
 Identities = 296/391 (75%), Positives = 332/391 (84%), Gaps = 2/391 (0%)
 Frame = +1

Query: 211 MPFGCVTLGDKKNYNQPSVTDRLYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 390
 MPFGC+TLG+KK+YN PSEVTD+YDLGQV+K+EEFCEIFRAKD+ T K++TCKKF K+DG
 sbjct: 1 MPFGCLTLGEKKDYNPSEVTDKYDLGQWKSEEFCEIFRAKDRNTLKMYTCKKFNKKDG 60

Query: 391 RKVRKAAKNEIGILKMVKHPNILLQVDFVTRKEYFIFLELATGREVFDWILDQGYYSER 570
 RKVRKAAKNEI ILKMVKH NILQLVD F T+KEYFIFLELATGREVFDWILDQGYYSER
 sbjct: 61 RKVRKAAKNEIMILKMVKHHNILLQVDAFETKKEYFIFLELATGREVFDWILDQGYYSER 120

Query: 571 DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLENGLIKEP 750
 DTSNV+RQVLEAVAYLHSLKIVHRNLK NLVY+NRLLK+SKIVISDF LAKLENGLIK+P
 sbjct: 121 DTSNMRQVLEAVAYLHSLKIVHRNLK--NLVYFNRLKHSKIVISDFQLAKLENGLIKDP 178

Query: 751 CGTPEYLAPEVWGRQRYGRPVDQWAGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRI 930
 CGTPEYLAPEV+GRQRYGRPVDQWAGVIMYILLSGNPPFY++ +E+D ++ DKNLF KI
 sbjct: 179 CGTPEYLAPEVIGRQRYGRPVDQWAGVIMYILLSGNPPFYDDGDEEDSDSRDKNLFRI 238

Query: 931 LAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEAEISHEWISGNAASDKNIKDG 1110
 L+GDYEFDSPYWDDIS +AK LV LMEV+QDQR+TA+EAI+HEWISGNAASDKNIKDG
 sbjct: 239 LSGDYEFDSPYWDDISDSAKTLVASLMEVDQDRLTAQEATAHEWISGNAASDKNIKDG 298

Query: 1111 CAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTAAQASAT--DTATPGAAGGATAAA 1284
 CAQIEKNFA+AKWKKAVRVTTLMKRLRA EQ T A+ A+ P GG+ AA
 sbjct: 299 CAQIEKNFAKAKWKKAVRVTTLMKRLRASEQDGTGASGLAAGATGGPPDPNMPGGSLLAA 358

Query: 1285 ASGATSAPEGDAARAASDNVAPADRSATPA 1377
 + + A S+ A A S P+
 sbjct: 359 -----SIKTALSEKAADAQTSTIPS 378

>gi|3122310|sp|Q63450|KCC1_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN
 KINASE TYPE I (CAM KINASE I)
 pir||S50193 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
 gb|AAA66944.1| (L26288) cam-like protein kinase [Rattus norvegicus]
 prf||2024225A Ca/calmodulin protein kinase I [Rattus norvegicus]
 Length = 374

Score = 310 bits (787), Expect = 4e-83
 Identities = 156/357 (43%), Positives = 226/357 (62%), Gaps = 4/357 (1%)
 Frame = +1

FIGURE 2J

Query: 250 YNQPSEVTDRLDGLGVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
 + Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
 Sbjct: 10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCTIAKALEGKEGSMENEIAV 69

Query: 430 LKMMKHPNIIQLVDVFTTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
 L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
 Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610 AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
 YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
 Sbjct: 130 KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDQWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPY 963
 + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPY
 Sbjct: 190 LAQKPYSKAVDCWSIGVIAIYILLCGYPPFYDE-----NDAKLFEQILKAIEYEFDSPY 241

Query: 964 WDDISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQAIEKNFARA 1143
 WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
 Sbjct: 242 WDDISDSAKDFIRHLMKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKKA VRVTTLMKRLRAPE--QSSTAAQASATDTATPGAAGGATAAAASGATSAP 1308
 KWK+A T +++ +R + S Q+AS + TP A G A P
 Sbjct: 302 KWKQAFNATAVVRHMRKLQLGTSQEGQGQTASHGELLTPTAGGPAAGCCCRDCCVEP 358

>gi|4502553|ref|NP_003647.1| calcium/calmodulin-dependent protein
 kinase I [Homo sapiens]
 sp|Q14012|KCC1_HUMAN CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (CAM KINASE I)
 pir||S57347 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
 gb|AAA99458.1| (L41816) cam kinase I [Homo sapiens]
 Length = 370

Score = 309 bits (784), Expect = 9e-83
 Identities = 156/357 (43%), Positives = 225/357 (62%), Gaps = 4/357 (1%)
 Frame = +1

Query: 250 YNQPSEVTDRLDGLGVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
 + Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
 Sbjct: 10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCTIAKEALEGKEGSMENEIAV 69

Query: 430 LKMMKHPNIIQLVDVFTTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
 L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
 Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610 AYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPEYLAPEV 783
 YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
 Sbjct: 130 KYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDQWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKILAGDYEFDSPY 963
 + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPY
 Sbjct: 190 LAQKPYSKAVDCWSIGVIAIYILLCGYPPFYDE-----NDAKLFEQILKAIEYEFDSPY 241

Query: 964 WDDISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQAIEKNFARA 1143
 WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
 Sbjct: 242 WDDISDSAKDFIRHLMKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

FIGURE 2K

Query: 1144 KWKAVRVTTLMKRLRAPE--QSSTAAQASATDTATPGAAGGATAAAASGATSAP 1308
 KWK+A T +++ +R + S Q+AS + TP A G A P
 Sbjct: 302 KWKQAFNATAVVRHMRKLQLGTSQEQGQQTASHGELLTPVAGGPAAGCCCRDCCVEP 358

>gi|3114436|pdb|1A06| Calmodulin-Dependent Protein Kinase From Rat
 Length = 332

Score = 303 bits (768), Expect = 7e-81
 Identities = 146/316 (46%), Positives = 213/316 (67%), Gaps = 2/316 (0%)
 Frame = +1

Query: 250 YNQPSEVTDRLGQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
 + Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
 Sbjct: 10 WKQAEIRDIDYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430 LKMKHPNIIQLVDVFTTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
 L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G+Y+ERD S ++ QVL+AV
 Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAV 129

Query: 610 AYLSLKIIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPPEYLAPEV 783
 YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
 Sbjct: 130 KYLHDLGIVHRDLKPENLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

Query: 784 VGRQRYGRPVDCWAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 963
 + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSPY
 Sbjct: 190 LAQKPYSKAVDQWSIGVIAIYILLGYPFFYDE-----NDAKLFEQILKAEYEFDSPY 241

Query: 964 WDDISQAAKDLVTRLMEVEQDQRTAAEEATISHEWISGNAASDKNIKDGVCAQIEKNFARA 1143
 WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
 Sbjct: 242 WDDISDSAKDFIRHLMKDPKRFTEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKAVRVTTLMKRLR 1191
 KWK+A T +++ +R
 Sbjct: 302 KWKQAFNATAVVRHMR 317

>gi|406113|gb|AAA19670.1| (L24907) protein kinase I [Rattus
 norvegicus]
 Length = 332

Score = 299 bits (758), Expect = 1e-79
 Identities = 146/316 (46%), Positives = 212/316 (66%), Gaps = 2/316 (0%)
 Frame = +1

Query: 250 YNQPSEVTDRLGQVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDGRKVRKAAKNEIGI 429
 + Q ++ D YD V+ T F E+ A+DK T KL K K+ + +NEI +
 Sbjct: 10 WKQAEIRDIDYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAV 69

Query: 430 LKMKHPNIIQLVDVFTTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAV 609
 L +KHPNI+ L D++ + ++ ++L +G E+FD I+++G Y+ERD S ++ QVL+AV
 Sbjct: 70 LHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGGYTERDRSRLIFQVLDAV 129

Query: 610 AYLSLKIIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPCGTPPEYLAPEV 783
 YLH L IVHR+LK ENL+YY+ ++SKI+ISDF L+K+E+ ++ CGTP Y+APEV
 Sbjct: 130 KYLHDLGIVHRDLKPENLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEV 189

FIGURE 2L

Query: 784 VGRQRYGRPVDCAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSFY 963
 + ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSFY
 Sbjct: 190 LAQKPYSKAVDCWSIGVIAYILLCGYPPFYDE-----NDAKLFEQILKAIEYEFDSFY 241

Query: 964 WDDISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQAQIEKNFARA 1143
 WDDIS +AKD + LME + ++R T E+A+ H WI+G+ A DKNI V QI+KNFA++
 Sbjct: 242 WDDISDSAKDFIRHLMKDPKRFRTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKS 301

Query: 1144 KWKAVRVTTLMKRLR 1191
 KWK+A T +++ +R
 Sbjct: 302 KWKQAFNRTAVVRHMR 317

>gi|9966875|ref|NP_065130.1| CamKI-like protein kinase [Homo sapiens]
 gb|AAG00534.1|AF286366_1 (AF286366) CamKI-like protein kinase [Homo sapiens]
 Length = 357

Score = 299 bits (757), Expect = 1e-79
 Identities = 142/332 (42%), Positives = 221/332 (65%), Gaps = 2/332 (0%)
 Frame = +1

Query: 256 QPSEVTDRYDLGQVIKTEEFCEIFRAKDKTGKLTCKKFQKRDGRKVRKAAKNEIGILK 435
 Q ++ ++ + + T F E+ A++K TGKL K K+ + + +NEI +L+
 Sbjct: 15 QAEDIKKIFEFKETLGTGAFSEVWLAEKATGKLFVAVKCIKKALKKGESSIENEIAVLR 74

Query: 436 MMKHPNQLVDFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAVAY 615
 +KH NI+ L D++ + ++ ++L +G E+FD I+++G+Y+E+D S ++RQVL+AV Y
 Sbjct: 75 KIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAVYY 134

Query: 616 LHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLE--NGLIKEPCGTPEYLAPEVVG 789
 LH + IVHR+LK ENL+YY++ + SKI+ISDF L+K+E ++ CGTP Y+APEV+
 Sbjct: 135 LHRMGIVHRDLKPENLLYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVLA 194

Query: 790 RQRYGRPVDCAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSFYWD 969
 ++ Y + VDCW+IGVI YILL G PPFY+E +D LF +IL +YEFDSFYWD
 Sbjct: 195 QKPYSKAVDCWSIGVIAYILLCGYPPFYDE-----NDSKLFEQILKAIEYEFDSFYWD 246

Query: 970 DISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQAQIEKNFARAKW 1149
 DIS +AKD + LME + ++R T E+A H WI+G+ A +KNI + V AQI KNFA++KW
 Sbjct: 247 DISDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKW 306

Query: 1150 KKAVRVTTLMKRLRAPEQSSTAAQASATDT 1245
 ++A T +++ +R S+ + +AS + +
 Sbjct: 307 RQAFNATAVVRHMRKLHLGSSLDSSNASVSSS 338

>gi|3893099|emb|CAA76937.1| (Y17917) calcium/calmodulin dependent
 protein kinase I [Drosophila melanogaster]
 gb|AAF59343.1| (AE003844) CamKI gene product [alt 2] [Drosophila melanogaster]
 Length = 405

Score = 288 bits (729), Expect = 3e-76
 Identities = 152/388 (39%), Positives = 243/388 (62%), Gaps = 21/388 (5%)
 Frame = +1

FIGURE 2M

Query: 238 DKKNYNQPSEVTDRLGQVIKTEEFCEIFRAKDKTT-GKLHTCKKFQKRDGRKVRKAAK 414
 D K N+ + ++Y+L ++ T F E+ A+ K + G+ K K+ + ++ +
 Sbjct: 17 DLKELNKQVSIEEKYNLHGLLTGAFSEVRLAESKDSPGEHFAVKIIDKKALKGKEESLE 76

Query: 415 NEIGILKM-----VKHPNIIQLVDVFTVTRKEYFIFLELATGREVFDWILD 549
 NEI +L+ + HPNI+QL++ + + + ++ +EL TG E+FD I++
 Sbjct: 77 NEIRVLRRFSANHFDGKCLNGTRLTHPNIVQLLETYEDKSKVYLMELVTGGELFDRIVE 136

Query: 550 QGYYSERDTSNVRQVLEAVAYLHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLE 729
 +G Y+E+D S+++RQ+LEAV Y+H +VHR+LK ENL+YY+ +SKI+ISDF L+K+E
 Sbjct: 137 KGSYTEKDASHLIRQILEAVDYMHEQGVVHRDLKPENLLYSPDDDSKIMISDFGLSKME 196

Query: 730 N-GLIKEPCGTPEYLAPEWGRQRYGRPVDCAIGVIMYILLSGNPPFYEEVEEDDYENH 906
 + G++ CGTP Y+APEV+ ++ YG+ VD W+IGVI YILL G PPFY+E +
 Sbjct: 197 DSGIMATACGTPGYVAPEVLAQKPYGKAVDWSIGVISYILLCGYPPFYDE-----N 248

Query: 907 DKNLFRKILAGDYEFDSPYWDISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAAS 1086
 D NLF +IL GD+EFDSPYWD+IS++AK + LM V ++R T ++A+ H WISGN AS
 Sbjct: 249 DANLFAQILKGDFFDSPYWDSESAKHFIKMLCVTVKRYTCKQALGHAWISGNEAS 308

Query: 1087 DKNIKDGVCAQIEKNFARAKWKAVRVTTLMKRLRAPEQSSTAAA----QSASATDTATP 1254
 +NI V Q++KNFA++HWK+A T+++++ +S + A ++S D+ TP
 Sbjct: 309 SRNIHGTVSEQLKKNFAKSRWKQAYYAATVIRQMORMALNSNSNANFDSSNSSNQDSTTP 368

Query: 1255 GAAGGATAAAASGATSAPEGDAARAAS 1338
 AA GA + + + + A KS
 Sbjct: 369 TAATGAWTSNVLSSQSQSVQSHAQEMNKS 396

>gi|4007153|emb|CAA19296.1| (AL023754) dJ272L16.1 (Rat Ca²⁺/Calmodulin
 dependent Protein Kinase LIKE protein) [Homo sapiens]
 Length = 460

Score = 286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256 QPSEVTDRLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
 Q + + + +V+ + F E+F K + TGKL K +K + + +NEI +LK
 Sbjct: 15 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCKIKSPAFR-DSSLENETAVLK 73

Query: 436 MKHPNIIQLVDVFTVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAVAY 615
 +KH NI+ L D++ + Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
 Sbjct: 74 KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILRGVYTEKDASLVIQQVLSAVKY 133

Query: 616 LHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEWGR 792
 LH IVHR+LK ENL+Y +NSKI+I+DF L+K+E NG++ CGTP Y+APEV+ +
 Sbjct: 134 LHENGIVHRDLKPENLLYLTPENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 193

Query: 793 QRYGRPVDCAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWD 972
 + Y + VDCW+IGVI YILL G PPFYEE E LF KI G YEF+SP+WDD
 Sbjct: 194 KPYSKAVDCWSIGVITYILLCGYPPFYETE-----SKLFEKIEGYEFESPFWD 245

Query: 973 ISQAADLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWK 1152
 IS++AKD + L+E + ++R T E+A+SH WI GN A ++I V QI+KNFA++KW+
 Sbjct: 246 ISESAKFICHILLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 305

FIGURE 2N

Query: 1153 KAVRVTTLMKRLRAPEQS---STAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAAR 1326
 ++ ++ +R + S T + ++ T AP D +
 Sbjct: 306 QAFNAAAVVHMRKLHNNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 365

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
 A + P P G S +GS+ S+ P GS+
 Sbjct: 366 ALPALTQLPCQHGRRPPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 411

>gi|4678722|emb|CAB41259.1| (AL049688) hypothetical protein [Homo sapiens]
 Length = 481

Score = 286 bits (724), Expect = 1e-75
 Identities = 157/408 (38%), Positives = 233/408 (56%), Gaps = 5/408 (1%)
 Frame = +1

Query: 256 QPSEVTDRLQGVIKTEEFCEIFRAKDKTGKLHTCKKFQKRDGRKVRKAAKNEIGILK 435
 Q + + + +V+ + F E+F K + TGKL K +K + + +NEI +LK
 Sbjct: 20 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLK 78

Query: 436 MVKHPNIIQLVDVVFVTRKEYFIFLELATGREVFDWILDQGYYSERDTSNVRQVLEAVAY 615
 +KH NI+ L D++ + Y++ ++L +G E+FD IL++G Y+E+D S V++QVL AV Y
 Sbjct: 79 KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKY 138

Query: 616 LHSLKIVHRNLKLENLVYNNRLKNSKIVISDFHLAKLE-NGLIKEPCGTPEYLAPEVWGR 792
 LH IVHR+LK ENL+Y +NSKI+I+DF L+K+E NG++ CGTP Y+APEV+ +
 Sbjct: 139 LHENGIVHRDLKPENLLYLTPPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQ 198

Query: 793 QRYGRPVDQWAGVIMYILLSGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSFYWDD 972
 + Y + VDCW+IGVI YILL G PPFYEE E LF KI G YEF+SP+WDD
 Sbjct: 199 KPYSKAVDCWSIGVITYILLCGYPPFYETE-----SKLFEKIKEGYEFESPFWDD 250

Query: 973 ISQAAKDLVTRLMEVEQDQRITAEAAISHEWISGNAASDKNIKDGVCQIEKNFARAKWK 1152
 IS++AKD + L+E + ++R T E+A+SH WI GN A ++I V QI+KNFA++KW+
 Sbjct: 251 ISESAKDFICHILLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 310

Query: 1153 KAVRVTTLMKRLRAPEQS---STAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAAR 1326
 +A ++ +R + S T + ++ T AP D +
 Sbjct: 311 QAFNAAAVVHMRKLHNNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSV 370

Query: 1327 AAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGSV 1464
 A + P P G S +GS+ S+ P GS+
 Sbjct: 371 ALPALTQLPCQHGRRPPTAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 416

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	229.1	6.5e-65	1
CE00022	CE00022 MAGUK_subfamily_d	105.3	5.5e-31	2
CE00287	CE00287 PTK_Eph_orphan_receptor	-71.4	0.0011	1
CE00292	CE00292 PTK_membrane_span	-87.6	0.00079	1
CE00291	CE00291 PTK_fgf_receptor	-125.1	0.13	1
CE00286	E00286 PTK_EGF_receptor	-159.5	0.3	1
CE00290	CE00290 PTK_Trk_family	-188.3	0.028	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-237.5	0.0016	1

FIGURE 20

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/2	117	152 ..	118	153 ..	4.3	0.35
CE00286	1/1	43	245 ..	1	263 []	-159.5	0.3
CE00292	1/1	26	259 ..	1	288 []	-87.6	0.00079
CE00290	1/1	29	266 ..	1	282 []	-188.3	0.028
CE00291	1/1	24	266 ..	1	285 []	-125.1	0.13
CE00287	1/1	24	284 ..	1	260 []	-71.4	0.0011
PF00069	1/1	37	286 ..	14	278 .]	229.1	6.5e-65
CE00022	2/2	182	286 ..	188	283 ..	100.8	1.2e-29
CE00016	1/1	3	357 ..	1	433 []	-237.5	0.0016

FIGURE 2P

1 AATGAAATCC TGTATCTACA AAAAAATTTT TAAAAATTAG CCAGTTGTGG
51 TGGTGTGCAC CTATGGTCCA GTCCTAGCTA CTCAGGAGGC TGAGGTGGGA
101 GGATCGCTTG AGCCCAGGAG GTTGAGGCTG GAATGAGCTG TGATCATTCC
151 ACTGCATTCC AGCCTGGGTG CCACTGCATT CCAGCCTGGG TGACAGAACA
201 GCTGGGCATG GTGCGGGTGC CTGTAATCCC AGCTGCGGTG GGAGGATCGT
251 TTGAGTTCAG GAGCTCTGGG CTGCAGTGCG CTATGCCAGT TGGGTGTCTA
301 CACTAAGTTT GGCATTAGTA TGGTGACTTC CTGGGAGCTA GAGCTCATCA
351 GGTTCCTTAA AGGAGGGGTG AAGCAACCAA GGTCAGAGAC GAAGCAGGTC
401 AAAACTCCTG TGCTGATCAG TAGTGGGCTT GTGCCATGA ATAGCCACTG
451 CACTCCAGCC TGGGCAACAT AGTGAGACTT GTCTCTAAAA AAAGAAAGAA
501 AGAAAGAAAA GAAAAGAAAA GAAATAGGTC TTCCAGAATC CCCCCCATGT
551 GTCCTGAATC AATCATAACC CCTCCTTTTC TCTTAGAAGG GACCATTATC
601 TGA CTCTGCT TATTTCTAG CTTTTCTTTA TAGCTCTACT GCTGTGTTTG
651 TATCCCCCTT ACGGGTTTTG TCTGCCTGTT TGA ACTCTAT CAATAGACTC
701 ATACTATATG TATTTCTTTG TGTCTTTTGG CACTTAACAC TGTGTAAGAG
751 TCACCAGGTG GTTGGGTATA GCTGTAGCTC CTTTGTTTCC ATTGCTATAT
801 AATATTCCAT TGTGTGACTC TACCACAATA CATCTGTGTG GTGGTGGTAT
851 TTGGTCTGTT TTCAATTTTT GCGGATTATG TATATGGCTA CTATGAGCAT
901 TGTATGACTG TCCTGATGCA CGAATATGTG CACTTCTGTA GGCACGTATT
951 TAGGATGCA ATTGCTGGTT CATAGGGTAT GTTTGTTTGA CTTTAGTGGT
1001 TTTACCAAAC TGCTTTACAA AGGGGAGTTT GCCCTCTCCT AGCAGTGCTC
1051 AC GTTCTTCA TATATCCACT AACACTTGTT AGCTCTAGAC CTTCAGAGAT
1101 GACTAGCAGG TGGGTGGGTG GTTATAGCCC CTTTCATCTG TAAAATAGCT
1151 GAAATTTAAA TAACTGTTT GATAAGCCTT TTTTGAATG TATAGAATAC
1201 AAAACTATTC CTTTATATAT CAGCTTAATA CATTTTTCAT TATGTAGGCT
1251 GTTGCACTTC AGGCAGCCAA GCTGAGTAGC TGGATGTCTA GCCAGAAAAG
1301 CAGGGGTAGG ATCTAAGCCT GCCTATCCTC TAGCCCCTCC TGGTATGGTC
1351 TCTGCCCCTA GCTTGGCCTG AGCCAGGTTG GGGTCTCCCA AAAGCAGCCC
1401 CTATGTTGTG GGAAGTGGA GAGTAGTACA GCTAAGCCAG ACCCCATTGT
1451 GCGCGCAGGT TAGAGCCTGG CAATGCCGTT TGGGTGTGTG ACTCTGGGCG
1501 ACAAGAAGAA CTATAACCAG CCATCGGAGG TGA CTGACAG ATATGATTTG
1551 GGACAGGTCA TCAAGACGTG AGTGCCGGGC CTGTGAGGCA AGGCTGGGTG
1601 GGCTGGTGAG CAGGGGCTAG GGAAGTGGCA GTGGAGTGCA GCTGATGCTA
1651 AGGCCAGGCC TGAGTGGGTG CCTGTGCGCT GCAGTGAGGA GTTTTGTGAA
1701 ATCTTCCGGG CCAAGGACAA GACGACAGGC AAGCTGCACA CCTGCAAGAA
1751 GTTCCAGAAG CGGGACGGCC GCAAGGTGCG GAAAGCTGCC AAGAACGAGA
1801 TAGGCATCCT CAAGATGTGA GTTTGAGGCC TGGGATTGGG GCGGGGTGGG
1851 AGGCAGCAGG GAAGGGCTTA GAGGGCAAGT GGCTCAGGC AGTCCCAGCC
1901 TCTGGCCAAT TAGTACTGCT GTGGCCACTG TGGTGACCAC AGCCTCTCCC
1951 AGGGGTTTCA CCAGCCCTAA CTA CTGCTC CCCTCCCTGT CGCCAGGGTG
2001 AAGCATCCCA ACATCCTACA GCTGGTGGAT GTGTTTGTGA CCCGCAAGGA
2051 GTACTTTATC TTCTGGAGC TGTGAGTGTG GGTCTGGGGA CCCAAGATTG
2101 CCCAGCGCCC AGGGCTTTCA CCTGTCCAC CCTCTGCAGC TAAGGAAACC
2151 CCCTTTCTGG ACCCTTGGCG TCCCAGGTCC CTGTGCCTTG CTCAGCCAGC
2201 TGCCTGGCGT AGGCAGCTCA CCCAAGTGCT CCTGCCCTAC CCCTGATTCT
2251 GCCCACGCCA GGCTCAGGGG CTGGTGTCCC TCAGGGCCAC GGGGAGGGAG
2301 GTGTTTGA CT GGATCCTGGA CCAGGGCTAC TACTCGGAGC GAGACACAAG
2351 CAACGTGGTA CGGCAAGTCC TGGAGGCCGT GGCTATTG CACTCACTCA
2401 AGATCGTGCA CAGGAATCTC AAGGTGAGGG CAGAGCCAGA GTCAAAGGGC
2451 CAGTTGGCAG CTGGGCTGGT GCTGGGGTGG GCAGCACCTC AGGGCCTTGG
2501 TCTAGCCTCC AAGGTCTCA TGGTGTCTTC TGCTACCCA CATGCTATTC
2551 TCACACCACA GCTGGAGAAC CTGGTTTACT ACAACCGCT GAAGAACTCG
2601 AAGATTGTCA TCAGTGACTT CCATCTGGCT AAGCTAGAAA ATGGCCTCAT
2651 CAAGGAGCCC TGTGGGACCC CCGAGTATCT GGGCAAGCAG GGGGTGGGGC
2701 AGGGGCAGGG GGATAATGGG GGGCAGCCTT CAGGGAGCTG CTCTGGGCAG
2751 GGGGAAAATG TGCTCATCTC AGGAAGCTGG TGTGGATGGT ACTGGACCTG
2801 GCTAGGCCTG ATACTGACCA GCAGATGGGC GCTGTGTTTG TAGCCCCAGA
2851 GGTGGTAGGC CGGCAGCGGT ATGGACGCC TGTGGACTGC TGGGCCATTG
2901 GAGTCATCAT GTACATCCTG TGAGTGGACA GATGGACAAG CAGGCTTGCA

FIGURE 3A

2951 GTCAGATGGG GTGGGGGCAT GTGTCTGTGG CCTTCTGTG TGACCCCTCC
 3001 CCCATGCAGG CTTTCAGGCA ACCCACCTTT CTATGAGGAG GTGGAAGAAG
 3051 ATGATTATGA GAACCATGAT AAGAATCTCT TCCGCAAGAT CCTGGCTGGT
 3101 GACTATGAGT TTGACTCTCC ATATTGGGAT GATATTTTCG AGGCAGGTGA
 3151 GGAGGTGCCT GCCCAGCACT TGGTAGAACG CAAGGGAGTG GGGAGGGTGT
 3201 CCTGCTCTCA TCTTCCTCTG TGGTATTCTG CTCTGTCCC CCAGCCCAT
 3251 TATCACCTCT AGACATTGAG ATGGGGTGCC CATGACTATC CCCTCCTTGG
 3301 TTTTGTCCAC AGCCAAAGAC CTGGTCACAA GGCTGATGGA GGTGGAGCAA
 3351 GACCAGCGGA TCACTGCAGA AGAGGCCATC TCCCATGAGT GGTGAGCAGG
 3401 GTCCAGGGGA GGGTGGGAGA GGCCAGGGTC CCCCTCACAC CCAGCAGCCC
 3451 CATCTTTGAG GCCTAGAAGG GGTGCAGGTA CCTAGAGCTC AGGGCAGCCC
 3501 AGAGGCTCTG CCTGGTAGTC CCTGGATGCC ACATAGAAGG GCTGAGCAGA
 3551 GTCTCCACAA AGGCTCATTC TCTCAGATCC AGACACACTT GCACCCCTTC
 3601 CAGGATTTCT GGCAATGCTG CTCTGATAA GAACATCAAG GATGGTGTCT
 3651 GTGCCCAGAT TGAAGAAGAAC TTTGCCAGGG CCAAGTGGAA GGTAAAGGCTT
 3701 GGATAACTCC CTTCTTGGCT CTATCCCAAG TATTGCTTCT GGCACCTAGT
 3751 TTCTTGCCCT CATCACACCC CTGCAGCCAC ACACAAGCTT TTCTCAGGCC
 3801 ATCAGTGTG GGTGTAGCCA CTGTGATTAC CTTAAGTAGG AGTGCTGAGC
 3851 AGCTGAGTAC TTGGCCCTGG GGTGGATGGA GGTGGCCGGG GGTACTATGG
 3901 AAGGAGTTTG GTTTGGTCAC TGCCAAGCAA TGGATCCAGC AAGCCTCACC
 3951 CTTAGCCTTT CTCCACTGTG CTCCTTTCAG AAGGCTGTCC GAGTGACCAC
 4001 CCTCATGAAA CGGCTCCGGG CACCAGAGCA GTCCAGCACG GCTGCAGCCC
 4051 AGTCGGCCTC AGCCACAGAC ACTGCCACCC CCGGGGCTGC AGGTGGGGCC
 4101 ACAGCTGCAG CTGCGAGTGG AGCTACCTCA GCCCCTGAGG GTGATGCTGC
 4151 TCGTGCTGCA AAGAGTGATA ATGTGGCCCC CGCAGACCGT AGTGCCACCC
 4201 CAGCCACAGA TGGAAAGTGC ACCCCAGCCA CTGATGGCAG TGTCAACCCA
 4251 GCCACCGATG GAAGCATCAC TCCAGCCACT GATGGGAGTG TCACCCAGC
 4301 CACTGACAGG AGCGTACTC CAGCCACTGA TGGGAGAGCC ACACCAGCCA
 4351 CAGAAGAGAG CACTGTGCCC ACCACCCAAA GCAGTGCCAT GCTGGCCACC
 4401 AAGGCAGCTG CCACCCCTGA GCCGGCTATG GCCCAGCCGG ACAGCACAGC
 4451 CCCAGAGGGC GCCACAGGCC AGGCTCCACC CTCTAGTAAA GGGGAAGAGG
 4501 CTGCTGGTTA TGCCCAGGAG TCTCAAAGGG AGGAGGCCAG CTGAGTAGGC
 4551 AGCCTGGTGA GGGGGGGCAG GGGATGGGCA GGAGGGTGGG AGAGTGGATG
 4601 AGGGGCTTCT CACTGTACAT AGAGTCACTG GCATGATGCC CTCGCTCCCC
 4651 CATGCCCCCA CATCCCAGTG GGGCATAACT AGGGGTACG GGAGAGCAGT
 4701 CTCGTCTCCT GTGTGTATGT GTGTGAGTGG TGGGCAGGCC AGTGGCAGGG
 4751 CCGGCCCCAG CCCCTGCATG GATTCTTGT GGCTTTTCTG TCTTTTGCTA
 4801 GCTTCACCAG TTTCTGTTCC TTGTGGGATG CTGCTCTAGG GATACTCAGG
 4851 GGGCTCCTGC TCTCCTTCCC CTTCCCTTCT TGCCCTACCA TTCCCCTAGG
 4901 CAGGCCCTGC AGGTCCCACA CTCTCCAGG CCTAAACTT GGGCGGCCTT
 4951 GCCCTGAGAG CTGGTCTCC AGCGAGGCCC TGTCAGCGGT CTTAGGCTCC
 5001 TGCACATGAA GGTGTGTGCC TGTGGTGTGT GGGCTGCTCT AGGAGCAGAT
 5051 ACAGGCTGGT ATAGAGGATG CAGAAAGGTA GGGCAGTATG TTTAAGTCCA
 5101 GACTTGGCAC ATGGCTAGGG ATACTGCTCA CTAGCTGTGG AGGTCCTCAG
 5151 GAGTGGAGAG AATGAGTAGG AGGGCAGAAG CTTCCATTTT TGTCTTCTCT
 5201 AAGACCCTGT TATTTGTGTT ATTTCTGCCC TTTCCGAGTC CTGCAGTGGG
 5251 CTGCCCTGTA CCCTGAACCT CATGAGCCTC TAAGGGAAAG GAGGAACAAT
 5301 TAGGACGTGG CAATGAGACC TGGCAGGGCA GAGTACAAGC CCAGCACCCA
 5351 GTGTCCCAGC CTTAATGGGT CCTTACCATG GGCCAAACAG GGAGGGCTGA
 5401 TACCTCCTTG CTCTTCTAG ATGCCACCT CCTACAATCT CAGCCCACAA
 5451 GTCCTCTCCA CCTAGGGGGC TTGCTGCATG GCAATAACTC ATAATTTGAT
 5501 TTGGAGGTTT GCCCTTTACA GGGGCAGATT TTCTGCTCAG TTCAACAATG
 5551 AAATGAAGAG GAACTCCCTC TTTCTACAGC TCACTTCTAT CAGAGGCCCA
 5601 GGTGCCTCAG AGCCACATTG AGTTGCTTTT TCTGGGATGA GGAAGTAGGG
 5651 TTAAACTCCC CAGTTTCTTG AGGGAGGCTC CTGACAGGTG CCCTTTGTCA
 5701 GACCCTACCA CAGCCTGGAT AGGCAGCCAC ATTGGTCCTC GCCCTTGCTC
 5751 GGCACTCCGT GGTGGTCTG CCCTTCTCCC TGCACTGCTG TGGGTCTGCT
 5801 CTGGTGTGTG AAGGTCGGTG GGTAACTGT GTGCCTACTG AACCTGGCAA
 5851 ATAAACATCA CCCTGCAAAG CCTCTGGCCA CCCTCTCGCC TTTGCTTCTT

FIGURE 3B

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5901 CTGTCCTACT GGGGAGGAGC CCCTGGAAGG CAGTGGGGAA GGGAGAGGCT
5951 GGGAGCAGGT TCACAAGTAG TGGCTGGGAG TAGTAGTGAA CAGTGCCCTG
6001 TGGATTTCTT GGGCTGAGGG TGAAGATCAT CCTCACCACA GTGTATTCTT
6051 CAATGGTGGT GGTGGTGGGG GTCCTCTGAA CTCTAGAAAT CCATGTGAGT
6101 AGTGGGTCTT GGGCTGCATT TGGACCAAGG AATACTCCCT GGGCTGAGAG
6151 CTAAGTAAG GGCTGCTGTT TTTGACTCCT GTTGACCGAG GAGCCTTACT
6201 CTTGATTTAG GCATAGAGCT GGAATCTACC TGGGCCAGCC AGCGCAAGGA
6251 CAGACCTGTC TCATAGCCAA AGATAGCTTC CCTGAGCTAG GGAGAGGGTG
6301 TAGGGTGAGC AATGCACAAA GATTCTATGC TGCTCTGTGT TGATTCCTTC
6351 TTTCTGTGAA CACCTGTGCT TTCCACCTAT GCCCCAAATG AAATCTCACT
6401 CTGGGTCTAT TTCAGCTGGA GCAGATCAGC TTTATATTAT GGGACTATGC
6451 ACAGGGTTTC TTCTGGGTAG AGGGAGTAAC ACTGCCACAG AACTAAGCC
6501 TAAAAACCCA AAAGTTGACT TACTCCAGCC CAGGTGGGCC TGGGTGAACT
6551 CACCAGGGAT GCTGCTCTCT GGGAGGACCT CAAAGATAAC CTCCTCAAGG
6601 ATAACCTCTC TGATGTGGGA ATAATAAAAA GGATTTGTTA GTCTCTAGTC
6651 TTTGAAGCAT CTGGGCCTCC AAAATTCCAA CCCTACTACA GTCTCAAGCA
6701 TAACTGATCC TCCTGAGAGC TAAGAGCTAA AGTCAGGGTA CTGGCCCTAG
6751 TGTCTCCAAA CTCGAAGGATA GTCATATCTT ACTTGATGA AGCCAAGGTT
6801 GGCCTGGGGT GACCTGAGGG ACTGGGGCCT ATGTGTCCAT CTTTCTAGAA
6851 TCGCCCCGAA CTGAGGACTG AGAGGGTAGG GTATTGTGGT CTATGGGAAC
6901 TCAGACCAT AGCGCATGGT CCATCACTGT CCAGAGCCCA AGGGACCCAT
6951 CGGGACCATT GTTCTATTCC CTTGCGGCTG CGGTTTTCTC TGCCTTGCC
7001 CAGCCTGCCT CGCGCCAGCT CTGGCATGGG ACCACAATGC GCTGCCTTGC
7051 CCTGGA AAAAG GGTCCAGCTG GCAGCCTCGC TGCTCCCCGC CTTGATATAA
7101 TGCTGCGCTC TCAAGTGGCA GGTCGAGTCT CCCCAGAGGA CGCCTGAGAG
7151 CGACCGCGCT CCGCCCAGGA TTCTCTACGG CCTCGGGGCC GCTAAGCCCC
7201 GCCCATAGTT CCGCCCATCC GAGAATTTGT CCAATCCAGG CGAAGTATTC
7251 ACGTCCGCC CAAAGTTTTG TGTGTCACT TCCGGCCCCG TCCAGGAAGT
7301 CGTGCTGCGG AGCCAAATTT GAAGCAAGCG GAGGCGCGGG GGCGCGTCTA
7351 CGAAGCCGGA CCTGTAGCAG TTTCTTTGCG TGCTGGGCC CCTTGAGTCC
7401 AGCCATCATG CCTATCCGTG CTCTGTGCAC TATCTGCTCC GACTTCTTCG
7451 ATCACTCCCG CGACGTGGCC GCCATCCACT GCGGCCACAC CTTCCACTTG
7501 CAGTGGTGAG TGACTGCAGT GTTGGGGCCC GGTGTTTGCC CG

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FEATURES:

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Start: 1473
Exon: 1473-1567
Intron: 1568-1684
Exon: 1685-1816
Intron: 1817-1996
Exon: 1997-2071
Intron: 2072-2284
Exon: 2285-2423
Intron: 2424-2561
Exon: 2562-2682
Intron: 2683-2843
Exon: 2844-2919
Intron: 2920-3009
Exon: 3010-3146
Intron: 3147-3312
Exon: 3313-3391
Intron: 3392-3603
Exon: 3604-3691
Intron: 3692-3980
Exon: 3981-4541
Stop: 4542

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FIGURE 3C

CHROMOSOME MAP POSITION:
 Bac Accession #: AC068701
 Chromosome: 3

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
234	T	A	Beyond ORF(5')			
328	T	C	Beyond ORF(5')			
1499	C	T	Exon	9	G	G
3022	T	C	Exon	217	N	N
3295	C	T	Intron			
4677	T	A	Beyond ORF(3')			
5583	C	T A	Beyond ORF(3')			
6242	G	C	Beyond ORF(3')			
7264	G	A	Beyond ORF(3')			

Context:

DNA
Position
 234

AATGAAATCCTGTATCTACAAAAAATTTTAAAAATTAGCCAGTTGTGGTGGTGTGCAC
 CTATGGTCCAGTCTAGCTACTCAGGAGGCTGAGGTGGGAGGATCGCTTGAGCCCAGGAG
 GTTGAGGCTGGAATGAGCTGTGATCATTCCACTGCATTCCAGCCTGGGTGCCACTGCATT
 CCAGCCTGGGTGACAGAACAGCTGGGCATGGTGCGGGTGCCTGTAATCCCAGC

[T,A]

GCGGTGGGAGGATCGTTTGAGTTCAGGAGCTCTGGGCTGCAGTGCCTATGCCAGTTGGG
 TGCTACACTAAGTTTGCCATTAGTATGGTGACTTCTGGGAGCTAGAGCTCATCAGGTT
 GCCTAAAGGAGGGGTGAAGCAACCAAGGTGAGAGACGAAGCAGGTCAAACTCCTGTGCT
 GATCAGTAGTGGGCTTGTCCTCATGAATAGCCACTGCACTCCAGCCTGGGCAACATAGTG
 AGACTTGTCTCTAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAATAGGTCTTCC

328

TTTTAAAAATTAGCCAGTTGTGGTGGTGTGCACCTATGGTCCAGTCTAGCTACTCAGGA
 GGCTGAGGTGGGAGGATCGCTTGAGCCCAGGAGGTTGAGGCTGGAATGAGCTGTGATCAT
 TCCACTGCATTCCAGCCTGGGTGCCACTGCATTCCAGCCTGGGTGACAGAACAGCTGGGC
 ATGGTGCAGGTGCTGTAATCCCAGCTGCGGTGGGAGGATCGTTTGAGTTCAGGAGCTCT
 GGGCTGCAGTGCGCTATGCCAGTTGGGTGTCTACACTAAGTTTGCCATTAGTATGGTGAC

[T,C]

TCCTGGGAGCTAGAGCTCATCAGGTTGCCTAAAGGAGGGGTGAAGCAACCAAGGTGAGAG
 ACGAAGCAGGTCAAACTCCTGTGCTGATCAGTAGTGGGCTTGTCCTCATGAATAGCCAC
 TGCACTCCAGCCTGGGCAACATAGTGAGACTTGTCTCTAAAAAAGAAAGAAAGAAAGAA
 AAGAAAGAAAGAAATAGGTCTTCCAGAAATCCCCCATGTGTCCTGAATCAATCATAA
 CCCCTCCTTTCTCTTAGAAGGGACCATTATCTGACTCTGCTATTTCTAGCTTTTCTT

1499

ACAAAATATTCCCTTATATATCAGCTTAATACATTTTTTCATATGTAGGCTGTTGCACT
 TCAGGCAGCCAAGCTGAGTAGCTGGATGTCTAGCCAGAAAAGCAGGGGTAGGATCTAAGC
 CTGCCTATCCTCTAGCCCCCTCCTGGTATGGTCTCTGCCCCTAGCTTGGCCTGAGCCAGGT
 TGGGGTCTCCAAAAGCAGCCCCTATGTTGTGGGGAAGTGAGAGTAGTACAGCTAAGCC
 AGACCCCATGTGCCCCGAGGTTAGAGCCTGGCAATGCCGTTTGGGTGTGTGACTCTGGG

[C,T]

GACAAGAAGAACTATAACCAGCCATCGGAGGTGACTGACAGATATGATTTGGGACAGGTC
 ATCAAGACGTGAGTGCCGGGCTGTGAGGCAAGGCTGGGTGGGCTGGTGAGCAGGGGCTA
 GGGAGTGGCAGTGGAGTGCAGCTGATGCTAAGGCCAGGCCTGAGTGGGTGCCTGTGCGC
 TGCAGTGAGGAGTTTGTGAAATCTTCCGGGCCAAGGACAAGACGACAGGCAAGCTGCAC
 ACCTGCAAGAAGTTCAGAAGCGGGACGGCCGAAGGTGCGGAAAGCTGCCAAGAACGAG

3022

GGCAGCCTTCAGGGAGCTGCTCTGGGCAGGGGGAAAATGTGCTCATCTCAGGAAGCTGGT

FIGURE 3D

GTGGATGGTACTGGACCTGGCTAGGCCTGATACTGACCAGCAGATGGGCGCTGTGTTTGT
AGCCCCAGAGGTGGTAGGCCGGCAGCGGTATGGACGCCCTGTGGACTGCTGGGCCATTGG
AGTCATCATGTACATCCTGTGAGTGGACAGATGGACAAGCAGGCTTGCAGTCAGATGGGG
TGGGGGCATGTGTCTGTGGCCTTTCTGTGTGACCCTTCCCCATGCAGGCTTTCAGGCAA
[T, C]
CCACCTTTCTATGAGGAGGTGGAAGAAGATGATTATGAGAACCATGATAAGAATCTCTTC
CGCAAGATCCTGGCTGGTGAATGACTTCTCCATATTGGGATGATATTTTCGAG
GCAGGTGAGGAGGTGCCTGCCAGCACTTGGTAGAACGCAAGGGAGTGGGGAGGGTGTCC
TGCTCTCATCTTCCTCTGTGGTATTCTGCTTCTGTCCCCAGCCATTATCACCTCTAG
ACATTGAGATGGGGTGCCCATGACTATCCCTCCTTGGTTTGTCCACAGCCAAAGACCT

3295 CCTTCCCCATGCAGGCTTTCAGGCAACCCACCTTTCTATGAGGAGGTGGAAGAAGATGA
TTATGAGAACCATGATAAGAATCTCTTCCGCAAGATCCTGGCTGGTGAATGAGTTTGA
CTCTCCATATTGGGATGATATTTTCGAGGCAGGTGAGGAGGTGCCTGCCAGCACTTGGT
AGAACGCAAGGGAGTGGGGAGGGTGTCTGCTCTCATCTTCCTCTGTGGTATTCTGCTTC
TGTCCTCCAGCCATTATCACCTCTAGACATTGAGATGGGGTGCCCATGACTATCCCT
[C, T]
CTTGGTTTTGTCCACAGCCAAAGACCTGGTCACAAGGCTGATGGAGGTGGAGCAAGACCA
GCGGATCACTGCAGAAGAGGCCATCTCCCATGAGTGGTGAGCAGGGTCCAGGGGAGGGTG
GGAGAGGCCAGGGTCCCCCTCACACCCAGCAGCCCATCTTTGAGGCTAGAAGGGGTGC
AGGTACCTAGAGCTCAGGGCAGCCAGAGGCTCTGCCTGGTAGTCCCTGGATGCCACATA
GAAGGGCTGAGCAGAGTCTCCAAAGGCTCATTCTCTCAGATCCAGACACACTTGACC

4677 CAAAGCAGTGCCATGCTGGCCACCAAGGCAGCTGCCACCCCTGAGCCGGCTATGGCCCAG
CCGGACAGCACAGCCCCAGAGGGCGCCACAGGCCAGGCTCCACCCTTAGTAAAGGGGAA
GAGGCTGCTGGTTATGCCAGGAGTCTCAAAGGGAGGAGGCCAGCTGAGTAGGCAGCCTG
GTGAGGGGGGGCAGGGGATGGGCAGGAGGGTGGGAGAGTGGATGAGGGGCTTCTCACTGT
ACATAGAGTCACTGGCATGATGCCCTCGCTCCCCATGCCCCACATCCCAGTGGGGCAT
[T, A]
ACTAGGGGTACGGGAGAGCAGTCTCGTCTCCTGTGTGTATGTGTGTGAGTGGTGGGCAG
GCCAGTGGCAGGGCCGGCCCCAGCCCTGCATGGATTCTTGTGGCTTTTCTGTCTTTTG
CTAGCTTACCAGTTTCTGTTCTTGTGGGATGCTGCTTAGGGATACTCAGGGGGCTCC
TGCTCTCCTTCCCTTCCCTTCTTGCTCACCATTCCCCTAGGCAGGCCCTGCAGGTCCC
ACACTCTCCAGGCCCTAACTTGGCGGCCTTGCCCTGAGAGCTGGTCCCTCCAGCGAGG

5583 AGGGAAAGGAGGAACAATTAGGACGTGGCAATGAGACCTGGCAGGGCAGAGTACAAGCCC
AGCACCCAGTGTCCCAGCCTTAATGGGTCTTACCATGGGCCAAACAGGGAGGGCTGATA
CCTCCTTGCTCTTCTAGATGCCACCTCCTACAATCTCAGCCCACAAGTCCCTCTCCACC
TAGGGGGCTTGTGCTGCAATAAATCATAATTTGATTTGGAGGTTTGCCCTTTACAGG
GGCAGATTTTCTGCTCAGTTCAACAATGAAATGAAGAGGAACCTCCCTCTTTCTACAGCTC
[C, T, A]
CTTCTATCAGAGGCCAGGTGCCTCAGAGCCACATTGAGTTGCTTTTCTGGGATGAGGA
AGTAGGGTTAAACTCCCAGTTTCTGAGGGAGGCTCCTGACAGGTGCCCTTTGTGAGAC
CCTACCACAGCCTGGATAGGCAGCCACATTGGTCTCGCCCTTGCTCGGCACTCCGTGGT
GGTCTGCCCTTCTCCCTGCATGCCTGTGGGTCTGCTCTGGTGTGTGAAGGTGGTGGGT
TAACTGTGTGCCTACTGAACCTGGCAAATAAACATCACCTGCAAAGCCTCTGGCCACCC

6242 GGAGAGGCTGGGAGCAGGTTCAAGTAGTGGCTGGGAGTAGTAGTGAACAGTGCCCTGT
GGATTTCTTGGGCTGAGGGTGAAGATCATCCTCACCACAGTGTATTCTCAATGGTGGTG
GTGGTGGGGTCTCTGAATCTAGAAATCCATGTGAGTAGTGGGTCTTGGGCTGCATTT
GGACCAAGGAATACTCCCTGGGCTGAGAGCTCAAGTAAGGGCTGCTGTTTTTACTCCTG
TTGACCGAGGAGCCTTACTCTTGATTTAGGCATAGAGCTGGAATCTACCTGGGCCAGCCA
[G, C]
CGCAAGGACAGACCCTGCTCATAGCCAAAGATAGCTTCCCTGAGCTAGGGAGAGGGTGT
GGGTGAGCAATGCACAAAGATTCTATGCTGCTGTGTGTGATTCTTCTTCTGTGAACA
CCTGTGCTTTCCACCTATGCCCCAAATGAAATCTCACTCTGGGTCTATTTAGCTGGAGC
AGATCAGCTTTATATTATGGGACTATGCACAGGGTTTCTTCTGGGTAGAGGGAGTAACAC
TGCCACAGATACTAAGCCTAAAAACCCAAAGTTGACTTACTCCAGCCCAGGTGGGCTG

FIGURE 3E

7264

CTATTCCCTTGCGGCTGCGGTTTTCTCTGCCTTGGCCCAGCCTGCCTCGCGCCAGCTCTG
GCATGGGACCACAATGCGCTGCCTTGCCCTGGAAAAGGGTCCAGCTGGCAGCCTCGCTGC
TCCCGCCTTGATATAATGCTGCGCTCTCAAGTGGCAGGTGAGTCTCCCCAGAGGACGC
CTGAGAGCGACCGCGCTCCGCCCAGGATTCTCTACGGCCTCGGGGCGCTAAGCCCCGCC
CATAGTTCCGCCCATCCGAGAATTTGTCCAATCCAGGCGAAGTATTCACGCTCCGCCCAA
[G,A]
GTTTTGTGTTGTCACTTCCGGCCCGCTCCAGGAAGTCGTGCTGCGGAGCCAAATTTGAAG
CAAGCGGAGGCGCGGGGCGCGTCTACGAAGCCGGACCTGTAGCAGTTTCTTTGGCTGCC
TGGGCCCCCTTGAGTCCAGCCATCATGCCTATCCGTGCTCTGTGCACTATCTGCTCCGACT
TCTTCGATCACTCCCGCGACGTGGCCGCCATCCACTGCGGCCACACCTTCCACTTGCACT
GGTGAGTGACTGCAGTGTGGGGCCCGGTGTTTGCCCG

FIGURE 3F